

Figure 1

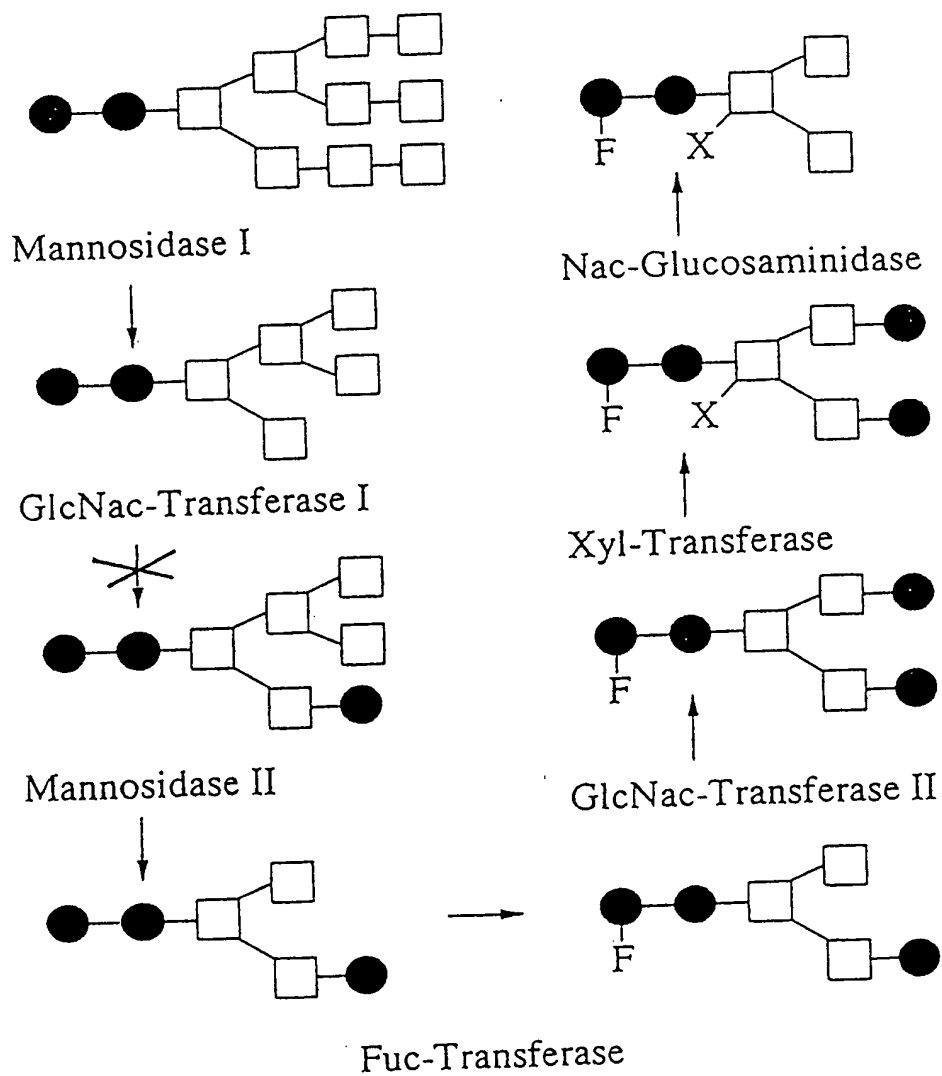


Figure 2

Al *GntI* cDNA

GAATTCGCGG CCGCCTGAGA AACCCCTCGAA TTCAATTTTCG CATTTGGCAG AG ATG 55
Met
1

AGA GGG AAC AAG TTT TGC TTT GAT TTA CGG TAC CTT CTC GTC GTG GCT 103
Arg Gly Asn Lys 5 Phe Cys Phe Asp Leu Arg Tyr Leu Leu Val Val Ala
10 15

GCT CTC GCC TTC ATC TAC ATA CAG ATG CGG CTT TTC GCG ACA CAG TCA 151
Ala Leu Ala Phe Ile Tyr Ile Gln Met Arg Leu Phe Ala Thr Gln Ser
20 25 30

GAA TAT GTA GAC CGC CTT GCT GCT GCA ATT GAA GCA GAA AAT CAT TGT 199
Glu Tyr Val Asp Arg Leu Ala Ala Ile Glu Ala Glu Asn His Cys
35 40 45

ACA AGT CAG ACC AGA TTG CTT ATT GAC AAG ATT AGC CAG CAG CAA GGA 247
Thr Ser Gln Thr Arg Leu Leu Ile Asp Lys Ile Ser Gln Gln Gln Gly
50 55 60 65

AGA GTA GTA GCT CTT GAA GAA CAA ATG AAG CAT CAG GAC CAG GAG TGC 295
Arg Val Val Ala Leu Glu Glu Gln Met Lys His Gln Asp Gln Glu Cys
70 75 80

CGG CAA TTA AGG GCT CTT GTT CAG GAT CTT GAA AGT AAG GGC ATA AAA 343
Arg Gln Leu Arg Ala Leu Val Gln Asp Leu Glu Ser Lys Gly Ile Lys
85 90 95

AAG TTA ATC GGA GAT GTG CAG ATG CCA GTG GCA GCT GTA GTT GTT ATG 391
Lys Leu Ile Gly Asp Val Gln Met Pro Val Ala Ala Val Val Val Met
100 105 110

GCT TGC AGT CGT ACT GAC TAC CTG GAG AGG ACT ATT AAA TCC ATC TTA 439
Ala Cys Ser Arg Thr Asp Tyr Leu Glu Arg Thr Ile Lys Ser Ile Leu
115 120 125

AAA TAC CAA ACA TCT GTT GCA TCA AAA TAT CCT CTT TTC ATA TCC CAG 487
Lys Tyr Gln Thr Ser Val Ala Ser Lys Tyr Pro Leu Phe Ile Ser Gln
130 135 140 145

GAT GGA TCA AAT CCT GAT GTA AGA AAG CTT GCT TTG AGC TAT GGT CAG 535
Asp Gly Ser Asn Pro Asp Val Arg Lys Leu Ala Leu Ser Tyr Gly Gln
150 155 160

CTG ACG TAT ATG CAG CAC TTG GAT TAT GAA CCT GTG CAT ACT GAA AGA 583
Leu Thr Tyr Met Gln His Leu Asp Tyr Glu Pro Val His Thr Glu Arg
165 170 175

CCA GGG GAA CTG GTT GCA TAC TAC AAG ATT GCA CGT CAT TAC AAG TGG 631
Pro Gly Glu Leu Val Ala Tyr Tyr Lys Ile Ala Arg His Tyr Lys Trp
180 185 190

GCA TTG GAT CAG CTG TTT CAC AAG CAT AAT TTT AGC CGT GTT ATC ATA 679
Ala Leu Asp Gln Leu Phe His Lys His Asn Phe Ser Arg Val Ile Ile
195 200 205

CTA GAA GAT GAT ATG GAA ATT GCT GCT GAT TTT TTT GAC TAT TTT GAG 727
Leu Glu Asp Asp Met Glu Ile Ala Ala Asp Phe Phe Asp Tyr Phe Glu
210 215 220 225

Figure 2 (continued)

GCT GGA GCT ACT CTT CTT GAC AGA GAC AAG TCG ATT ATG <u>GCT ATT TCT</u> Ala Gly Ala Thr Leu Leu Asp Arg Asp Lys Ser Ile Met Ala Ile Ser 230 235 240	775
<u>TCT TGG AAT GAC AAT GGA</u> CAA AGG CAG TTC GTC CAA GAT CCT GAT GCT Ser Trp Asn Asp Asn Gly Gln Arg Gln Phe Val Gln Asp Pro Asp Ala 245 250 255	823
CTT TAC CGC TCA <u>GAC TTT TTT CCT GGT CTT GGA TGG</u> ATG CTT TCA AAA Leu Tyr Arg Ser Asp Phe Phe Pro Gly Leu Gly Trp Met Leu Ser Lys 260 265 270	871
TCA ACT TGG TCC GAA CTA TCT CCA AAG TGG CCA AAG GCT TAC TGG GAT Ser Thr Trp Ser Glu Leu Ser Pro Lys Trp Pro Lys Ala Tyr Trp Asp 275 280 285	919
GAC TGG CTA AGG CTG AAA GAA AAT CAC AGA GGT CGA CAA TTT ATT CGC Asp Trp Leu Arg Leu Lys Glu Asn His Arg Gly Arg Gln Phe Ile Arg 290 295 300 305	967
CCA GAA GTT TGC AGA ACG TAC AAT TTT GGT GAG CAT GGT TCT AGT TTG Pro Glu Val Cys Arg Thr Tyr Asn Phe Gly Glu His Gly Ser Ser Leu 310 315 320	1015
GGG CAG TTT TTT AAG CAG TAT CTT GAG CCA ATT AAG CTA AAT GAT GTC Gly Gln Phe Phe Lys Gln Tyr Leu Glu Pro Ile Lys Leu Asn Asp Val 325 330 335	1063
CAG GTT GAT TGG AAG TCA ATG GAC CTA AGT TAC CTT TTG GAG GAC AAC Gln Val Asp Trp Lys Ser Met Asp Leu Ser Tyr Leu Leu Glu Asp Asn 340 345 350	1111
TAT GTG AAA CAC TTT GGC GAC TTG GTT AAA AAG GCT AAG CCC ATC CAC Tyr Val Lys His Phe Gly Asp Leu Val Lys Lys Ala Lys Pro Ile His 355 360 365	1159
GGA GCT GAT GCT GTT TTG AAA GCA TTT AAC ATA GAT GGT GAT GTG CGT Gly Ala Asp Ala Val Leu Lys Ala Phe Asn Ile Asp Gly Asp Val Arg 370 375 380 385	1207
ATT CAG TAC AGA GAC CAA CTA GAC TTT GAA GAT ATC GCT CGA CAG TTT Ile Gln Tyr Arg Asp Gln Leu Asp Phe Glu Asp Ile Ala Arg Gln Phe 390 395 400	1255
GGC ATT TTT GAA GAA TGG AAG GAT GGT GTA CCA CGG GCA GCA TAT AAA Gly Ile Phe Glu Glu Trp Lys Asp Gly Val Pro Arg Ala Ala Tyr Lys 405 410 415	1303
GGG ATA GTA GTT TTC CGG TTT CAA ACA TCT AGA CGT GTG TTC CTT GTT Gly Ile Val Val Phe Arg Phe Gln Thr Ser Arg Arg Val Phe Leu Val 420 425 430	1351
TCC CCT GAT TCT CTT CGA CAA CTT GGA GTT GAA GAT ACT TAG Ser Pro Asp Ser Leu Arg Gln Leu Gly Val Glu Asp Thr End 435 440 445	1393
CGAAGATATG ATTGGAGCCT GAGCAACAAT TTAGACTTAT TTGGTAGGAT ACATTTGAAA	1453
GAGCTGACAC GAAAAGTATG ACTACCACTA GCTACATGCA ACATTTTAAT GTTAATGGAA	1513
GGAACCCACT GCTTATTGTT GGAATGGATG AATCATCACC ACATCCTATT ATTCAAGTTT	1573
ACAAACATAA AGAGGAAATG TTGCCCTATA AAAACAAATT TTTTGTTTCT AAGAAGGAAC	1633
GTTACGATTA TGAGCAACTT TGGCGGCCGC GAATTC	1669

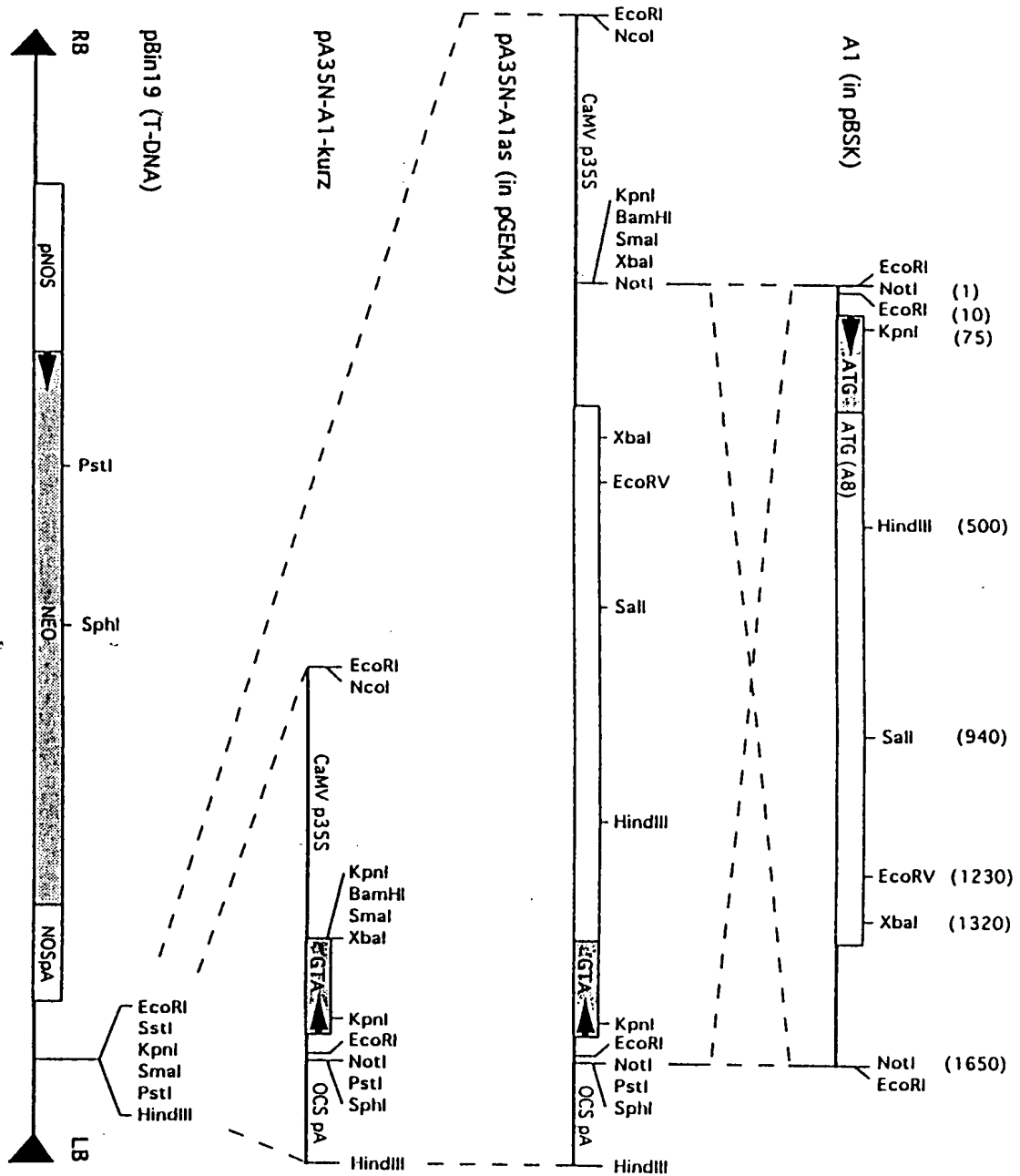
Figure 3A

Hu	Ra	Mo	Ce	St
35 (59)	36 (57)	35 (59)	33 (57)	
	92 (95)	91 (94)	38 (57)	Hu
		90 (93)	38 (57)	Ra
			38 (58)	Mo

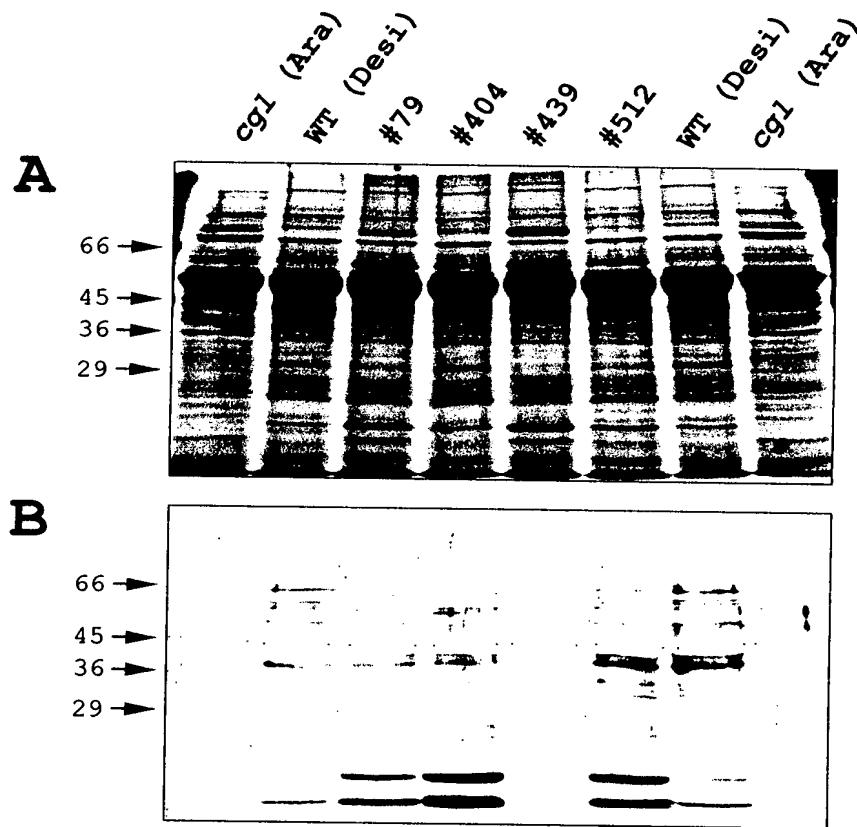
Figure 3B

A_Stb-A1	1	MRGNKFCF	DLRYLL	AA	AFIYIOMRLFATQSEY	VDRLAAAIEAENHCT
B_Ntb-A9	1	MRGNKFCCE	RYLLI	AA	AFIYIOMRLFATQSEY	ADRLAAAIEAENHCT
C_Atb-Full	1	..MA	ISCDLR	LLIE	AAFMFIYIOMRLF	QTOSEYADRLAAIEAENHCT
A_Stb-A1	51	SQTRLLID	KIS	QOGR	IVALEEOMK	QDOECROLRALVQDLESKGIKKLI
B_Ntb-A9	51	SQTRLLID	KIS	QOGR	IVALEEOMK	QDOECROLRALVQDLESKGIKKLI
C_Atb-Full	49	SOMRGLID	IS	KQSR	IVALEEOMK	NRQDELVOLKDLQTFEKKGIKKLI
A_Stb-A1	101	GVVOMPVA	AAVVVMACSR	DYLERT	IKSILKYOTS	VASKYPLFISODGSSNP
B_Ntb-A9	101	GVVOMPVA	AAVVVMACSR	DYLERT	IKSILKYOTS	VASKYPLFISODGSSNP
C_Atb-Full	99	QGGOMPVA	AAVVVMACSR	DYLERT	IKSILKYOTS	VASKYPLFISODGSSNP
A_Stb-A1	151	DVRKLALS	YGLTYMOHLD	EPVHTERPGEL	AYYKIARHYKWALDQLFH	
B_Ntb-A9	151	DVRKLALS	YGLTYMOHLD	EPVHTERPGEL	AYYKIARHYKWALDQLFH	
C_Atb-Full	149	AVSKLS	YGLTYMOHLD	EPVHTERPGEL	AYYKIARHYKWALDQLFH	
A_Stb-A1	201	KHNFSRVI	ILEDDEMEIA	ADFFDYFEAGATLLDRDKS	SIMAISSWNDNGOMQ	
B_Ntb-A9	201	KHNFSRVI	ILEDDEMEIA	ADFFDYFEAGATLLDRDKS	SIMAISSWNDNGOMQ	
C_Atb-Full	199	KHNFSRVI	ILEDDEMEIA	ADFFDYFEAGATLLDRDKS	SIMAISSWNDNGOMQ	
A_Stb-A1	251	FVQDEP	DALYRSDFFPGLGWMLSKSTW	SELSPKWPKAYWDDWLRLKENHRG		
B_Ntb-A9	251	FVQDEP	DALYRSDFFPGLGWMLSKSTW	SELSPKWPKAYWDDWLRLKENHRG		
C_Atb-Full	249	FVQDEP	DALYRSDFFPGLGWMLSKSTW	SELSPKWPKAYWDDWLRLKENHRG		
A_Stb-A1	301	ROFIRPEVC	RTYNFGEHGSSLG	OFFKOYLEPIKLN	DVQVDWKSMDLSYLL	
B_Ntb-A9	301	ROFIRPEVC	RTYNFGEHGSSLG	OFFKOYLEPIKLN	DVQVDWKSMDLSYLL	
C_Atb-Full	299	ROFIRPEVC	RTYNFGEHGSSLG	OFFKOYLEPIKLN	DVQVDWKSMDLSYLL	
A_Stb-A1	351	EDNYVKH	EGDLVKKAKPIHG	ADAVLKAFNIDG	DVRIQYRDQD	DFENIARO
B_Ntb-A9	351	EDNYVKH	EGDLVKKAKPIHG	ADAVLKAFNIDG	DVRIQYRDQD	DFENIARO
C_Atb-Full	349	EGNYTKY	ESGLVQAP	PIQGSDLV	LKAQNIKDD	DRIRYKQDQDFENIARO
A_Stb-A1	401	FGIFEW	KDGVPR	AAAYKGIVVFR	QTSRRVFLVSP	DSLRQOLGIEDT
B_Ntb-A9	401	FGIFEW	KDGVPR	AAAYKGIVVFR	QTSRRVFLVSP	DSLRQOLGIEDT
C_Atb-Full	399	FGIFEW	KDGVPR	AAAYKGIVVFR	QTSRRVFLVSP	DSLRQOLGIEDT

Figur 4



Figur 5



Figur 6

